

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 18:00:15 ; Search time 15 Seconds
(without alignments)
96.134 Million cell updates/sec

Title: US-09-300-612-1
Perfect score: 84
Sequence: 1 LKAMDTPPLWKTE 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	63	75.0	237	2	A42013		alpha-1-B-glycoprotein
2	46	54.8	1213	2	A54063		TATA-binding prote
3	44	52.4	695	2	E75099		hypothetical prote
4	44	52.4	777	2	T38769		hypothetical prote
5	44	52.4	1327	2	T09402		immunoglobulin-lik
6	43	51.2	341	2	AB0644		probable glycosyl
7	43	51.2	687	2	D86314		hypothetical prote
8	43	51.2	932	1	A31898		hydroxymethylgluta
9	42	50.0	115	2	D71194		hypothetical prote
10	42	50.0	398	2	A81717		hypothetical prote
11	42	50.0	453	2	T04646		conserved hypothet
12	42	50.0	564	1	VHXPMV		aspartate transami
13	42	50.0	662	2	A29900		major structural n
14	41	48.8	151	1	S30146		fasciclin I precur
15	41	48.8	339	2	JC5882		ribosomal protein
16	41	48.8	349	2	JC5881		myocyte enhancer f
17	41	48.8	411	2	AE2152		myocyte enhancer f
18	41	48.8	707	2	F86925		two-component sens
19	41	48.8	967	2	S58360		probable acyl-CoA
20	41	48.8	975	2	T03004		lanthibiotic Pep5 b
21	41	48.8	1172	2	T00065		hydroxyribonuclea
22	41	48.8	1559	2	T07757		hypothetical prote
23	40	47.6	97	2	S59888		probable DNA (cyto
24	40	47.6	205	2	S26854		C4 protein - tomat
25	40	47.6	205	2	A40525		microfilarial sheat
26	40	47.6	209	2	T43565		proline-rich sheat
27	40	47.6	209	2	B40049		type III secretion
28	40	47.6	210	2	S21428		virC-region hypoth
29	40	47.6	225	2	C70045		hypothetical prote
							two-component resp

30	40	47.6	231	2	F69977	two-component resp
31	40	47.6	309	2	H72626	probable 2-oxoacid
32	40	47.6	337	2	A97084	uncharacterized pr
33	40	47.6	406	2	C83867	Xaa-Pro dipeptidas
34	40	47.6	422	2	D86446	hypothetical prote
35	40	47.6	560	2	T02404	probable beta-gluc
36	40	47.6	609	2	S65208	probable membrane
37	40	47.6	1184	2	D86387	probable protein P
38	40	47.6	1215	2	E70614	hypothetical prote
39	40	47.6	3570	2	T45025	mucin MUC5B, trach
40	39.5	47.0	365	2	F87552	dprA protein (impo
41	39.5	47.0	631	2	A57286	probable serine/th
42	39	46.4	242	2	AD1928	hypothetical prote
43	39	46.4	256	1	WNBEFN	28K protein - suid
44	39	46.4	258	2	T23957	hypothetical prote
45	39	46.4	268	2	S31010	gene 65 protein -

ALIGNMENTS

RESULT 1

A42013
alpha-1-B-glycoprotein - North American opossum (fragments)
C:Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opo
C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 31-Dec-1993
C:Accession: A42013
R:Catanesse, J.J.; Kress, L.F.
Biochemistry 31, 410-418, 1992
A:Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to
A:Reference number: A42013; MUID:92118834; PMID:1731898
A:Accession: A42013
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-237 <CAT>
A:Cross-references: GB:J05356
C:Keywords: glycoprotein

Query Match 75.0%; Score 63; DB 2; Length 237;
Best Local Similarity 80.0%; Pred. No. 0.0087;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDTPPLWKTE 15
Db 1 LKAMDTPPLWKTE 15
||||| |||||

RESULT 2

A54063
TATA-binding protein-associated factor II - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 21-Jul-2000
C:Accession: A54063
R:Verrijzer, C.P.; Yokomori, K.; Chen, J.L.; Tjian, R.
Science 264, 933-941, 1994
A:Title: Drosophila TAF-II 150: similarity to yeast gene TSM-1 and specific binding t
A:Reference number: A54063; MUID:94233377; PMID:8178153
A:Accession: A54063
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1213 <VER>
A:Cross-references: GB:X79243; NID:g541664; PIDN:CAA55830.1; PID:g541665
C:Genetics:
A:Gene: Flybase:Taf150
A:Cross-references: Flybase:FBgn0011836

Query Match 54.8%; Score 46; DB 2; Length 1213;
Best Local Similarity 53.3%; Pred. No. 31;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LKAMDTPPLWKTE 15
Db 620 LSAMDSPVLWRLD 634
||||| |||||

RESULT 3

E75099

Hypothetical protein PAB1590 - *Pyrococcus abyssi* (strain Orsay)C:Species: *Pyrococcus abyssi*

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C:Accession: E75099

R:Anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome structure

A:Reference number: A75001

A:Accession: E75099

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-695 <KAW>

A:Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50098.1; PID:el51599

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB1590

Query Match 52.4%; Score 44; DB 2; Length 695;

Best Local Similarity 54.5%; Pred. No. 35;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AMDPTPLWIK 13

Db 561 ANDPPPMWLE 571

RESULT 4

T38769

Hypothetical protein SPAC3H8.11 - fission yeast (*Schizosaccharomyces pombe*)C:Species: *Schizosaccharomyces pombe*

C:Date: 20-Oct-2000 #sequence_revision 08-Dec-2000 #text_change 08-Dec-2000

C:Accession: T38769; T38072

R:Gentiles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, January 1996

A:Reference number: Z21810

A:Accession: T38769

A:Molecule type: DNA

A:Residues: 1-105 <GEN>

A:Cross-references: EMBL:Z69086; NID:gl177658; PIDN:CAA93168.1; PID:gl177669; GSPDB:GN00

A:Experimental source: strain 972h; cosmid c3H8

R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, April 1996

A:Reference number: Z21767

A:Accession: T38072

A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 90-777 <CON>

A:Cross-references: EMBL:Z70690; NID:gl256511; PIDN:CAA94619.1; PID:g3859771; GSPDB:GN00

A:Experimental source: strain 972h; cosmid c1F3

C:Genetics:

A:Gene: spac1f3.01; SPDB:SPAC3H8.11; SPDB:SPAC1F3.01

A:Map position: 1

Query Match

Best Local Similarity 52.4%; Score 44; DB 2; Length 777;

Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMDPTPLWIKTE 15

Db 212 SVDETEPIWSTE 224

RESULT 5

T09402

Immunoglobulin-like protein IGSF1 - human

C:Species: *Homo sapiens* (man)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: T09402

R:Mazzarella, R.; Pengue, G.; Jones, J.; Jones, C.; Schlessinger, D.

Genomics 48, 157-162, 1998

A:Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xq25

A:Reference number: Z16665; MUID:98190514; PMID:9521868

A:Accession: T09402

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1327 <MAZ>

A:Cross-references: EMBL:AF034198; NID:g2645889; PIDN:AAC52057.1; PID:g2645890

C:Genetics:

A:Gene: Igsf1

A:Map position: Xq25

Query Match

Best Local Similarity 52.4%; Score 44; DB 2; Length 1327;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPLWIKT 14

Db 25 MDPQPELWIES 35

RESULT 6

AB0644

Probable glycosyl hydrolase STY1249 [imported] - *Salmonella enterica* subsp. *enterica*C:Species: *Salmonella enterica* subsp. *enterica* serovar TyphiA:Note: This species has also been called *Salmonella typhi*

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: AB0644

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,

A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* se

A:Reference number: AB0502; PMID:11677608

A:Accession: AB0644

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD08333.1; PID:gi6502378; GSPDB:GN00176

C:Genetics:

A:Gene: STY1249

Query Match

Best Local Similarity 51.2%; Score 43; DB 2; Length 341;

Matches 8; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

QY 2 KAMDPTP---PLWIKT 14

Db 217 RAIDPRPAGSPYWLKT 233

RESULT 7

DB6314

Hypothetical protein F2H15.14 - *Arabidopsis thaliana*C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 30-Jun-2002

C:Accession: DB6314

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: AB6141; MUID:21016719; PMID:11130712

A:Accession: DB6314

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-687 <STO>

A; Gene: PAB1020

Query Match 50.0%; Score 42; DB 2; Length 453;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 MDPTPLWIK 13
DB 238 IDPTPEQWVK 247

RESULT 12

VHXPWV

major structural nucleoprotein - Machupo virus

N:Alternate names: Machopocapsid protein

C:Species: Machupo virus

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999

C:Accession: S18042

R:Griffiths, C.; Wilson, S.M.; Clegg, J.C.S.

submitted to the EMBL Data Library, October 1991

A:Description: Sequence of the nucleocapsid gene of Machupo virus: close relationship w

A:Reference number: S18042

A:Accession: S18042

A:Molecule type: genomic RNA

A:Residues: 1-564 <GRI>

A:Cross-references: EMBL:X62616; NID:G60621; PIDN:CAA44486.1; PID:G60622

C:Genetics:

A:Map position: segment S

C:Superfamily: arenavirus major nucleoprotein

C:Keywords: nucleocapsid; nucleoprotein

Query Match 50.0%; Score 42; DB 1; Length 564;
Best Local Similarity 46.7%; Pred. No. 58;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIKTE 15
DB 368 VKKLDPTWTLWDIE 362

RESULT 13

A29900

fasciclin I precursor - American bird grasshopper

C:Species: Schistocerca americana (American bird grasshopper)

C:Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 01-Dec-2000

C:Accession: A29900; A31817

R:Zinn, K.; McAllister, L.; Goodman, C.S.

Cell 53, 577-587, 1988

A:Title: Sequence analysis and neuronal expression of fasciclin I in grasshopper and Dro

A:Reference number: A29900; MUID:88223351; PMID:3370670

A:Accession: A29900

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-662 <ZIN>

A:Cross-references: GB:M20544; GB:J03787; NID:g160846; PID:g160847

R:Snow, P.M.; Zinn, K.; Harrelson, A.L.; McAllister, L.; Schilling, J.; Bastiani, M.J.;

Proc. Natl. Acad. Sci. U.S.A. 85, 5291-5295, 1988

A:Title: Characterization and cloning of fasciclin I and fasciclin II glycoproteins in t

A:Reference number: A94202; MUID:88276943; PMID:2839842

A:Accession: A31817

A:Molecule type: mRNA

A:Residues: 25-42 <SNO>

A:Cross-references: EMBL:M20544; EMBL:J03787

Query Match 50.0%; Score 42; DB 2; Length 662;
Best Local Similarity 58.3%; Pred. No. 70;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPLWIT 12
DB 104 LSELDGNPLWIT 115

RESULT 14

S30146

ribosomal protein S13, cytosolic - maize

C:Species: Zea mays (maize)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S30146

R:Joanin, P.; Gigot, C.; Philipps, G.

Plant Mol. Biol. 21, 701-704, 1993

A:Title: cDNA nucleotide sequence and expression of a maize cytoplasmic ribosomal pro

A:Reference number: S30146; MUID:93192530; PMID:8448368

A:Accession: S30146

A:Molecule type: mRNA

A:Residues: 1-151 <JOA>

A:Cross-references: EMBL:X62455; NID:g288058; PIDN:CAA44311.1; PID:g288059

C:Superfamily: rat ribosomal protein S13; eubacterial ribosomal protein S15 homology

C:Keywords: protein biosynthesis; ribosome

F:2-151/Product: ribosomal protein S13 #status predicted <MAT>

F:82-148/Domain: eubacterial ribosomal protein S15 homology <ES15>

Query Match 48.8%; Score 41; DB 1; Length 151;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 TPPLWIKT 14
DB 21 TPPTWIKT 28

RESULT 15

JC5882

myocyte enhancer factor 2B-2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 16-Jul-1999

C:Accession: JC5882

R:Morisaki, T.; Sermsuvitayawong, K.; Byun, S.H.; Matsuda, Y.; Hidaka, K.; Morisaki,

J. Biochem. 122, 939-946, 1997

A:Title: Mouse Mef2b gene: Unique member of MEF2 gene family.

A:Reference number: JC5881; MUID:98104045; PMID:9443808

A:Accession: JC5882

A:Molecule type: DNA

A:Residues: 1-339 <MOR>

A:Cross-references: DDBJ:D87828

C:Comment: This factor plays a differentiation of myocytes, including cardiomyocytes.

C:Genetics:

A:Gene: Mef2b

A:Map position: 8

C:Superfamily: serum response factor DNA-binding domain homology

F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 48.8%; Score 41; DB 2; Length 339;
Best Local Similarity 61.5%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AMDPTPLWIKTE 15
DB 281 ASPPTPPVSIKSE 293

Search completed: June 27, 2003, 18:02:39
Job time : 16 secs